OM of: US-09-494-297-2 to: GenEmbl:* out_format : pfs

Date: Jun 6, 2001 10:59 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn1_1/USPTO_spool/US09494297/runat_06062001_115734_12308/app_query.fasta_1.825
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=US09494297_@CGN1_1_7604 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-494-297-2
Query length: 757
Database: GenEmbl:*
Database sequences: 1283235
Database length: -1216004940
Search time (sec): 2987.740000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	! Documentation ..
gb_ba3:SPU49397	-	1965.50	1843.52	1.8e-94	10826	! U49397 Streptococcus pyogenes
gb_ba3:STRPRTNF	+	633.50	597.92	4.3e-25	2845	! L10919 Streptococcus pyogenes
gb_ba1:AF009908	+	611.00	576.82	6.5e-24	2801	! AF009908 Streptococcus pyogene
gb_ba3:SPSFB	+	603.00	571.10	1.4e-23	2263	! X67947 S.pyogenes Sfb gene for
gb_ba2:GGU31115	+	523.00	496.38	2.0e-19	2066	! U31115 Group G streptococcus f
gb_ba1:AF009914	+	272.50	275.93	3.7e-07	321	! AF009914 Streptococcus pyogenes
gb_ba1:AF009913	+	262.50	266.71	1.2e-06	313	! AF009913 Streptococcus pyogenes
gb_ba1:AF009910	+	241.50	246.54	1.6e-05	326	! AF009910 Streptococcus pyogenes
gb_ba1:AF009920	+	222.50	228.05	0.0002	348	! AF009920 Streptococcus pyogenes
gb_ba1:AF009917	+	211.50	219.59	0.0005	278	! AF009917 Streptococcus pyogenes
gb_ba1:AF009911	+	211.50	218.66	0.0006	310	! AF009911 Streptococcus pyogenes
gb_ba1:AF009918	+	210.50	217.74	0.0006	309	! AF009918 Streptococcus pyogenes
gb_ba1:AF009915	+	209.50	216.80	0.0007	309	! AF009915 Streptococcus pyogenes
gb_ba1:AF009912	+	205.50	213.81	0.0011	282	! AF009912 Streptococcus pyogenes
gb_ba1:AF009919	+	204.50	212.11	0.0013	308	! AF009919 Streptococcus pyogenes
gb_ba1:AF009909	+	202.50	211.01	0.0015	281	! AF009909 Streptococcus pyogenes
gb_ba1:AF009916	+	185.00	195.32	0.0115	255	! AF009916 Streptococcus pyogenes
gb_ba3:SEFNZGEN	+	180.00	172.44	0.2170	2127	! X99995 S.equi fnz gene. 1/1997
gb_pat1:AR083961	+	178.00	168.52	0.3584	2694	! AR083961 Sequence 2 from paten
gb_pat1:AR083960	+	178.00	159.58	1.13	7650	! AR083960 Sequence 1 from paten
gb_ba1:AF043131	+	178.00	158.24	1.34	8946	! AF043131 Moraxella catarrhalis
gb_pat2:AX067453	+	177.00	142.62	9.93	49617	! AX067453 Sequence 28 from Pat
gb_ba1:AF043133	+	176.00	166.56	0.4611	2718	! AF043133 Moraxella catarrhalis
gb_ba3:SPU31980	+	164.00	152.94	2.64	3552	! U31980 Streptococcus pyogenes
gb_ba2:AP000992	-	162.50	113.00	443.49	318850	! AP000992 Thermoplasma volcan
gb_ba1:AF120104	+	160.00	140.29	13.41	10020	! AF120104 Lactobacillus reuter
gb_ba2:LLU04468	+	159.00	146.93	5.72	4133	! U04468 Lactococcus lactis sex
gb_htg19:AL139040	+	159.00	114.67	358.06	178460	! AL139040 Homo sapiens chromo
gb_ba2:BACHSPN	+	155.00	141.25	11.84	5160	! D44498 Bacillus subtilis hspN
gb_pr4:AF134726	-	155.00	110.81	587.58	180283	! AF134726 Homo sapiens BAC cl
gb_ba1:AF188483	+	152.00	135.16	25.88	7551	! AF188483 Photorhabdus luminesc
gb_pr6:AP000503	-	151.50	112.56	469.73	100000	! AP000503 Homo sapiens genomi
gb_ba2:CDTOXBA	+	151.00	134.67	27.57	7164	! Z23277 C.difficile gene for to
gb_htg1:AC005505	+	151.00	106.46	1.0e+03	192929	! AC005505 Plasmodium falcipar
gb_htg1:AC005139	-	151.00	104.03	1.4e+03	256172	! AC005139 Plasmodium falcipar
gb_pat1:AR071281	+	150.00	139.78	14.30	3531	! AR071281 Sequence 1 from paten
gb_ba1:AF071083	+	150.00	139.39	15.05	3698	! AF071083 Streptococcus pyogene
gb_pr9:HUMMHHSP	+	149.00	141.14	12.02	2700	! M59828 Human MHC class III HSP
gb_ba3:SAU5646	+	149.00	137.88	18.25	3948	! AJ005646 Staphylococcus aureus
gb_pat1:AR067712	+	149.00	136.55	21.65	4612	! AR067712 Sequence 8 from paten
gb_ba3:STACNA	+	148.00	137.21	19.90	3827	! M81736 Staphylococcus aureus d
gb_pat1:AR067706	+	148.00	137.21	19.90	3827	! AR067706 Sequence 1 from pa
gb_ba1:AE002147	-	147.00	119.50	192.89	27093	! AE002147 Ureaplasma urealy
gb_pat1:A18434	+	146.00	136.16	22.75	3468	! A18434 Hybrid DNA molecule
gb_pat1:A18436	+	146.00	133.72	31.12	4612	! A18436 assembled sequence f

seq_name: gb_ba3:SPU49397

seq_documentation_block:
LOCUS SPU49397 10826 bp DNA BCT 19-DEC-1998
DEFINITION Streptococcus pyogenes MsmR (msmR) gene, partial cds; LepA (lepA), Cpa (cpa), and Nra (nra) genes, complete cds; SsbA (ssbA) gene, partial cds; and unknown genes.
ACCESSION U49397
VERSION U49397.1 GI:4028947
KEYWORDS .
SOURCE Streptococcus pyogenes.
ORGANISM Streptococcus pyogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 10826)
AUTHORS Podbielski,A., Woischnik,M., Leonard,B.A.B. and Schmidt,K.H.
TITLE Characterization of nra, a global negative regulator gene in group A streptococci
JOURNAL Mol. Microbiol. 31 (1999) In press
REFERENCE 2 (bases 1 to 10826)
AUTHORS Podbielski,A. and Woischnik,M.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1996) RWTH Aachen, Institute of Medical Microbiology, Pauwelsstrasse 30, Aachen, Nrw, Federal Republic of Germany, 52074

FEATURES Location/Qualifiers

source 1. .10826
/organism="Streptococcus pyogenes"
/strain="CS101"
/db_xref="taxon:1314"

gene <1. .630
/gene="msmR"

CDS <1. .630
/gene="msmR"
/function="multiple sugar metabolism regulator"
/codon_start=1
/transl_table=11
/product="MsmR"
/protein_id="AAC97150.1"
/db_xref="GI:4033713"
/translation="DLVKLGNPQLLKQEINRIPLSSITSSSISALRAEKNLTVIYLTR
LLEFSFVENTDVAKHYSLVKYYMALNEEASDLLKVLRIRCAAIIHFSESLTNKSISDK
RQMYNSVLHYVDSHLYSKLKVSDIAKRLYVSESHLRSVFKKYSNVSLQHYILSTKIKE
AQLLLKRGIPVGEVAKSLYFYDTTHFHKIFKKYTGISSKDYLAKYRDNI"

repeat_region 697. .730
/note="putative transcription terminator"
/rpt_type=inverted

CDS complement(790. .1377)
/note="ORF 2"
/codon_start=1
/transl_table=11
/product="unknown"
/protein_id="AAC97151.1"
/db_xref="GI:4033714"
/translation="MRKYWKMLFSVVMMLTMLAFNQTVLAKDSTVQTSISVENVLERA
GDSTPFSIALESIDAMKTIEEITIAGSGKASFSPLNFTTVGQYTYRVYQKPSQNKDYQ
ADTTVFDVLVYVTYDEDGTLVAKVISRRAGDEEKSAITFKPKRLVKPIPPRQPDIPKT
PLPLAGEVKSLLGILSIVLLGLLVLLYVKKLKSRL"

CDS complement(1394. .3169)
/note="similar to electron transfer flavorprotein 1 of Methylophilus electron; ORF 3"
/codon_start=1
/transl_table=11
/product="unknown"
/protein_id="AAC97152.1"
/db_xref="GI:4033715"
/translation="MKKNKLLLATAILATALGMASMSQNIKAETAGVIDGSTLVVKKT
FPSYTDDNVLMPKADYSFKVEADDNAKGKTKDGLDIKPGVIDGLENTKTIRYSNSDKI

TAKEKSVNFEFANVKFPGVGVYRYTVAEVNGNKAGITYDSQQWTVDVYVVNKEGGGFE
VKYIVSTEVGQSEKKPVLFKNSFDTTSLKIEKQVTGNTGEHQRLFSFTLLLTPNECFE
KGQVVNILQGGETKKVVIGEEYSFTLKDKGSVTLSQLPVGIEYKLTEEDVTKDGYKTS
ATLKDGEQSSTYELGKDHKTDKSADEIVVTNKRDTQVPTGVVGTLAPFAVLSIVAIGG
VIYITKRKKAQVISQRMMMTIVQVINKAIDTLILIFCLVVLFLAGFGLWDSYHLYQQA
DASNFKKFKTAQQQPKFEDLLALNEDVIGWLNIPGTHIDYPLVQGKTNLEYINKAVDG
SVAMSGSLFLDTRNHNDFTDDYSLIYGHHMAGNAMFGEIPKFLKKNFFNKHNKAIIET
KERKKLTVTIFACLKTDAFDQLVFNPNAITNQDQQRQLVDYISKRSKQFKPVKLKHHT
KFVAFSTCENFSTDNRVIVVGTIQE"

gene complement(3191. .3712)
/gene="lepA"

CDS complement(3191. .3712)
/gene="lepA"
/note="ORF 4; similar to Staphylococcus aureus signal peptidase 1"
/codon_start=1
/transl_table=11
/product="LepA"
/protein_id="AAC97149.1"
/db_xref="GI:4033712"
/translation="MTNYLNRLNENSLFKAFIRLVLKISIIGFLGYILFQYVFGVMII
NTNDMSPALSAGDGVLYYRLADRSHINDVVVYEVDNTLKVGRIAAQAGDEVNFTQEGG
LLINGHPPEKEVPYLTYPHSSGPNFPYKVPTGTYFILNDYREERLDSRYYGALPINQI
KGKISTLLRVRGI"

gene complement(3705. .6180)
/gene="cpa"

CDS complement(3705. .5933)
/gene="cpa"
/note="collagen-binding protein of group A Streptococci"
/codon_start=1
/transl_table=11
/product="Cpa"
/protein_id="AAC97148.1"
/db_xref="GI:4033711"
/translation="MQKRDKTNYGSANNKRRQTTIGLLKVFLTFVALIGIVGFSIRAF
GAEEQSVPNRQSSIQDYPWYGYDSYPKGYPDYSPLKTYHNLKVNLEGSKDYQAYCFNL
TKHFPSKSDSVRSQWYKKLEGTNENFIKLADKPRIEDGQLQQNILRILYNGYPNNRNG
IMKGIDPLNAILVTQNAIWYTDSAQINPDESFKTEARSNGINDQQLGLMRKALKELID
PNLGSKYSNKTPSGYRLNVFESHDKPFQNLLSAEYVPDTPPKPGEEPPAKTEKTSVII
RKYAEGDSKLLEGATLKLSQIEGSGFQEKDFQSNSLGETVELPNGTYTLTETSSPDGY
KIAEPIKFRVENKKVFIVQKDGSQVENPNKEVAEPYSVEAYNDFMDEEVLSGFTPYGK
FYYATNKDKSSQVVYCFNADLHSPPDSYDSGETINPDTSTMKEVKYTHTAGSDLFKYA
LRPRDTNPEDFLKHIKKVIEKGYKKKGDSYNGLTETQFRAATQLAIYYFTDSADLKTL
KTYNNGKGYHGFESMDEKTLAVTKELITYAQNGSAPQLTNLDFFVPNNSKDQSLIGTE
CHPDDLVDVIRMEDKKQEVIPVTHSLTVKKTVVGELGDKTKGFQFELELKDKTGQPIV
NTLKTNNQDLVAKDGKYSFNLKHGDTIRIEGLPTGYSYTLKEAEAKDYIVTVDNKVSQ
EAQSVGKDITEDKKVTFENRKDLVPPTGLTTDGAIYLWLLLLVPLGLLVWLFGRKGLK
ND"

-10_signal complement(5972. .5977)
/gene="cpa"
/note="promoter 1"

-35_signal complement(5997. .6102)
/gene="cpa"
/note="promoter 1"

-10_signal complement(6138. .6148)
/gene="cpa"
/note="extended promoter 2"

-35_signal complement(6161. .6166)
/gene="cpa"
/note="promoter 2"

-10_signal 6231. .6241
/gene="nra"
/note="extended promoter 2"

gene 6231. .7898
/gene="nra"

-35_signal 6297. .6302
/gene="nra"
/note="promoter 1"

-10_signal 6315. .6325
/gene="nra"
/note="extended promoter 1"

CDS 6363. .7898
/gene="nra"
/note="negative regulator of group A Streptococci"
/codon_start=1
/transl_table=11
/product="Nra"
/protein_id="AAC97147.1"
/db_xref="GI:4028948"
/translation="MPYVKKKKDSFLVETYLEQSIRDKSELVLLLFKSPTIIFSHVAK
QTGLTAVQLKYYCKELDDFFGNNLDITIKKGKIICCFVKPVKEFYLHQLYDTSTILKL
LVFFIKNGTSSQPLIKFSKKYFLSSSSAYRLRESLIKLLREFGLRVSKNTIVGEEYRI
RYLIAMLYSKFGIVIYPLDHLDNQIIYRFLSQSATNLRTSPWLEEPFSFYNMLLALSW
KRHQFAVSIPQTRIFRQLKKLFIYDCLTRSSRQVIENAFSLTFSQGDLDYLFLIYITT
NNSFASLQWTPQHIETCCHIFEKNDTFRLLLEPILKRLPQLNHSKQDLIKALMYFSKS
FLFNLQHFVIEIPSFSLPTYTGNSNLYKALKNIVNQWLAQLPGKRHLNEKHLQLFCSH
IEQILKNKQPALTVVLISSNFINAKLLTDTIPRYFSDKGIHFYSFYLLRDDIYQIPSL
KPDLVITHSRLIPFVKNDLVKGVTVAEFSFDKPDYSIASIQNLIYQLKDKKYQDFLNE
QLQ"

-10_signal 8006. .8016
/note="ORF 5; extended -10 signal"

CDS 8024. .8857
/note="ORF 5"
/codon_start=1
/transl_table=11
/product="unknown"
/protein_id="AAC97154.1"
/db_xref="GI:4033717"
/translation="MDKIIKSIAQSGAFRAYVLDSTETVALAQEKHNTLSSSTVALGR
TLIANQILAANQKGDSKITVKVIGDSSFGHIISVADTKGHVKGYIQNTGVDIKKTETG
EVLVGPFMGNGHFVTIIDYGTGNPYTSTTPLITGEIGEDFAYYLTESEQTPSAIGLNV
LLDENDKVKVAGGFMVQVLPEASEEEIARYEKRLQEMPAISHLLASKNHVDALLEAIY
GDEPYKRLSEEPLSFQCDCSRERFEAALMTLPKADLQAMIDEDKGAEIVCQFCGTKLP
I"

CDS 8884. .9861
/note="ORF 6; similar to Azospirillum brasilense nifR3 gene"
/codon_start=1
/transl_table=11
/product="unknown"
/protein_id="AAC97155.1"
/db_xref="GI:4033718"
/translation="MIKLNSSFRIGDVEIPHRTVLAPMAGVTNSAFRTIAKEFGAGLV
VMEMISEKGLLYNNEKTLHMLHIDENEHPMSIQLFGGDAEGLKRAADFIQTNTKADIV
DINMGCPVNKVVKNEAGAKWLRDPDKIYHIVKEVTSVLDIPLTVKMRTGWADSSLAVE
NALAAESAGVSALAMHGRTREQMYTGTCDHETLARVSKAITKIPFIGNGDVRSVQDAK
FMIEEIGVDAVMIGRAAMNNPYLFTQINHFFETGQELPDLPFAKKLDIAKDHLKRLIN
LKGETIAVREFRGLAPHYLRGTAGAAKVRGAVSRAETLAEVEAIFETVR"

CDS 9881. .10522
/note="similar to Lactobacillus acidophilus dA/dG-kinase"
/codon_start=1
/transl_table=11
/product="unknown"
/protein_id="AAC97156.1"
/db_xref="GI:4033719"
/translation="MLIVLAGTIGAGKSSLAAALGEHLGTDVFYEAVDNNPVLDFYYQ
DPKKYAFLLQIYFLNKRFKSIKEAYQADNNILDRSIFEDELFLKLNYKNGNVTKTELD
IYQELLANMLEELEGMPKKRPDLLIYIDVSFDKMLERIEKRGRSFEQVDGNPSLEQYY
HQVHGEYPTWYEDYKVSPKMKIDGNSLDFVQNPQDLATVLKMIDTKLKELHLL"

repeat_region 10598. .10681
/note="putative transcription terminator"
/rpt_type=inverted

gene complement(10782. .>10826)
/gene="ssbA"

CDS complement(10782. .>10826)

alignment_scores:
Quality: 1965.50 Length: 737
Ratio: 3.412 Gaps: 13
Percent Similarity: 78.155 Percent Identity: 54.410

alignment_block:
US-09-494-297-2 x SPU49397/rev ..

Align seg 1/1 to reverse of: SPU49397 from: 1 to: 10826


20 SerLysAsnSerLysArg.....PheThrValThrLeuValGlyValPh 34
5903 AGCGCTAACAACAAACGACGACAAACGACGATCGGATTACTGAAAGTATT 5854
34 eLeuMetIlePheAlaLeuValThrSerMetValGlyAlaLysThrValP 51
5853 TTTGACGTTTGTAGCTCTGATAGGAATAGTAGGGTTTTCTATCAGAGCGT 5804
51 heGlyLeuValGluSerSerThrProAsnAlaIleAsnProAspSerSer 67
5803 TCGGAGCTGAAGAACAATCAGTACCAAAT.....AGACAAAGCTCAATT 5760
68 SerGluTyrArgTrpTyrGlyTyrGluSerTyrValArgGlyHisProTy 84
5759 CAAGATTATCCGTGGTATGGCTATGATTCTTATCCTAAAGGCTACCCAGA 5710
84 rTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlyS 101
5709 CTATAGTCCGTTAAAGACTTACCATAATTTAAAAGTAAATTTAGAGGGAA 5660
101 erArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaProLeu 117
5659 GTAAGGATTATCAAGCATACTGCTTTAATTTAACAAAACATTTTCCATCC 5610
118 GlySerAspSerSerValLysLysTrpTyrLysLysHisAspGlyIleSe 134
5609 AAGTCAGATAGTGTTAGATCACAATGGTATAAAAAACTTGAAGGAACTAA 5560
134 rThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAspGluL 151
5559 TGAAAACTTTATCAAGTTAGCAGATAAACCAAGAATAGAAGACGGACAGT 5510
151 euAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAla 167
5509 TACAACAAAATATATTGAGGATTCTCTATAATGGATATCCTAATAATCGT 5460
168 AsnGlyIleMetGluGlyLeuGluProLeuAsnAlaIleArgValThrGl 184
5459 AATGGGATAATGAAAGGGATAGATCCTCTAAACGCTATTTTAGTGACTCA 5410
184 nGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnProAspG 201
5409 AAATGCTATTTGG...TATACTGATTCAGCTCAAATT...AATCCGGATG 5366
201 luSerPheLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeu 217
5365 AAAGTTTTAAAACAGAAGCTCGAAGTAATGGTATTAATGACCAGCAGTTA 5316
218 SerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaTh 234
5315 GGCTTAATGCGAAAAGCTTTAAAAGAACTAATTGATCCAAACTTAGGGTC 5266
234 rLysMetProLysGlnValProAspAspPheGlnLeuSerIlePheGluS 251
5265 AAAATATTCGAATAAAACTCCATCAGGTTATCGGTTAAATGTATTTGAAT 5216
251 erGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSer 267
5215 CTCATGAT.....AAGCCTTTCCAAAATCTTTTGAGT 5184
268 GlyGlyLeuValProThrLysProProThrProGlyAspProProMetPr 284
5183 GCTGAGTATGTTCCGGATACTCCCCCAAAACCAGGAGAAGAG.....CC 5140
284 oProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleG 301
5139 TCCGGCTAAAACTGAAAAAACATCAGTCATTATCAGAAAATATGCGGAAG 5090
301 lyAspTyrSerLysLeuGluGlyAlaThrLeuGlnLeuThrGlyAsp 317
5089 GTGAC...TCTAAACTTCTAGAGGGAGCAACCTTAAAGCTTTCTCAAATT 5043
318 AsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGlyGl 334
5042 GAAGGAAGTGGTTTTCAAGAAAAAGACTTTCAAAGTAATAGTTTAGGAGA 4993
334 uArgIleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerP 351
4992 AACTGTCGAATTACCAAATGGGACTTATACCTTAACAGAAACATCATCTC 4943
351 roAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaGly 367
4942 CAGATGGATATAAAATTGCGGAGCCGATTAAGTTTAGAGTAGAGAATAAA 4893
368 LysValTyrThrIle...IleAspGlyLysGlnIleGluAsnProAsnLy 383
4892 AAAGTATTTATCGTCCAAAAAGATGGTTCTCAAGTGGAAAATCCAAACAA 4843
383 sGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluP 400
4842 AGAAGTAGCAGAGCCATACTCAGTGGAAGCGTATAATGACTTTATGGATG 4793
400 heSerValLeuThr...ThrGlnAsnTyrAlaLysPheTyrTyrAlaLys 415
4792 AAGAAGTACTCTCGGGTTTTACTCCATACGGAAAATTCTATTACGCTACA 4743
416 AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLy 432
4742 AATAAGGATAAAAGTTCACAAGTTGTCTACTGCTTCAATGCTGATTTACA 4693
432 sSerProProAspSerGluAspGlyGlyLysThrMetThrProAspPheT 449
4692 CTCACCACCTGACTCATATGATAGTGGTGAGACTATAAATCCAGATACTA 4643
449 hrThr...GlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPhe 464
4642 GTACGATGAAAGAAGTCAAGTACACACATACGGCAGGTAGTGACTTGTTT 4593
465 LysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHi 481
4592 AAATATGCGCTAAGACCGAGAGATACAAATCCAGAAGACTTCTTAAAGCA 4543
481 sIleLysLysValIleGluLysGlyTyrArgGluLysGlyGlnAlaIleG 498
4542 CATTAAAAAAGTAATTGAAAAAGGCTACAAGAAAAAAGGTGATAGC.... 4497
498 luTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAla 514
4496 ..TATAATGGATTAACAGAAACACAGTTTCGCGCGGCTACTCAGCTTGCT 4449
515 IleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeu..... 529
4448 ATCTATTATTTTACAGACAGTGCTGACTTAAAAACCTTAAAAACTTATAA 4399
530 ....LysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuA 544
4398 CAATGGGAAAGGTTACCATGGATTTGAATCTATGGATGAAAAAACCCTAG 4349
544 laValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProProGln 560
4348 CTGTCACAAAAGAATTAATTACTTATGCTCAAAATGGCAGTGCCCCTCAA 4299
561 LeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLe 577
4298 CTAACAAATCTTGATTTCTTCGTACCTAATAATAGCAAAGACCAATCTCT 4249
577 uIleGlyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetG 594
4248 TATTGGGACAGAATGCCATCCAGATGATTTGGTTGACGTGATTCGTATGG 4199
594 luAspLysLys...GluValIleProValThrHisAsnLeuThrLeuArg 609
4198 AAGATAAAAAGCAAGAAGTTATTCCAGTAACTCACAGTTTGACAGTGAAA 4149
610 LysThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGl 626

```
 4148 AAAACAGTAGTCGGTGAGTTGGGAGATAAAACTAAAGGCTTCCAATTTGA 4099

  626 uIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysT 643
      |:::|||||||||:::::::      :::   :::   :::|||:::|||||
 4098 ACTTGAGTTGAAAGATAAAACTGGACAGCCTATTGTTAACACTCTAAAAA 4049

  643 hrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeu 659
      ||::::::  . :::|||      ||||||||||||   ::::::||||||
 4048 CTAATAATCAAGATTTAGTAGCTAAAGATGGGAAATATTCATTTAATCTA 3999

  660 LysHisGlyGluSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTy 676
      |||||||||:::::::::   ::::::||||||||   ||||||||||
 3998 AAGCATGGTGACACCATAAGAATAGAAGGATTACCGACGGGATATTCTTA 3949

  676 rLeuValLysGluThrAspSerGluGlyTyrLysValLysValAsnSerG 693
      |   :::||||||:::::::::::::   |||   |||   |||:::::::
 3948 TACTCTGAAAGAGGCTGAAGCTAAGGATTATATAGTAACCGTTGATAACA 3899

  693 lnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAspGlu 709
      ::          :::|||                ||||||:::|||:::.
 3898 AAGTTAGTCAAGAAGCGCAGTCAGTAGGTAAGGATATAACAGAAGACAAA 3849

  710 ThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAs 726
      ::::::||||||||||:::|||:::   |||  ||||||||:::
 3848 AAAGTCACTTTTGAAAACCGAAAAGATCTTGTCCCACCAACTGGTTTGAC 3799

  726 pGlnLysIleAsnGlyTyrLeuAlaLeuIleValIleAlaGlyIleSerL 743
                    ||||||   |||:::::::::::::   ::::::|
 3798 AACAGATGGGGCTATCTATCTTTGGTTGTTATTACTTGTTCCACTTGGGT 3749

  743 euGlyIleTrp 746
      ||   :::|||
 3748 TATTGGTTTGG 3738

seq_name: gb_ba3:STRPRTNF

seq_documentation_block:
LOCUS       STRPRTNF     2845 bp    DNA             BCT       24-NOV-1993
DEFINITION  Streptococcus pyogenes fibronectin-binding protein (prtF) gene,
            complete cds.
ACCESSION   L10919
VERSION     L10919.1  GI:425479
KEYWORDS    adhesin; fibronectin-binding protein; protein F; prtF gene.
SOURCE      Streptococcus pyogenes (strain JRS75) DNA.
  ORGANISM  Streptococcus pyogenes
            Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 2845)
  AUTHORS   Sela,S., Aviv,A., Burstien,I., Tovi,A., Caparon,M.G. and Hanski,E.
  TITLE     Protein F: An adhesin of Streptococcus pyogenes binds fibronectin
            via two distinct domains
  JOURNAL   Mol. Microbiol. 10, 1049-1055 (1993)
  MEDLINE   95020565
FEATURES             Location/Qualifiers
     source          1. .2845
                     /organism="Streptococcus pyogenes"
                     /strain="JRS75"
                     /db_xref="taxon:1314"
     gene            425. .2404
                     /gene="prtF"
     CDS             425. .2404
                     /gene="prtF"
                     /codon_start=1
                     /transl_table=11
                     /function="binds fibronectin"
                     /product="protein F"
                     /protein_id="AAA26964.1"
                     /db_xref="GI:425480"
                     /translation="MFVRGEKMNNKIFLNKEASFLAHTKRKRRFAVTLVGVFFMLLAC
                     AGAIGFGQVAYAADEKTVPSHSSPNPEFPWYGYDAYGKEYPGYNIWTRYHDLRVNLNG
                     SRSYQVYCFNIQSNYPSQKNSFIKNWFKKIEGNGKSFVDYAHTTKLGKEELEQRLLSL
                     LYNAYPNDANGYMKGLEHLNAITVTQYAVWHYSDNSQYQFETLWESEAKEGKISRSQV
                     TLMREALKKLIDPNLEATAVNKIPSGYRLNIFESENEAYQNLLSAEYVPDDPPKPGET
                     SEHNPKTPELDGTPIPEDPKHPDDNLEPTLPPVMLDGEEVPEVPSESLEPALPPLMPE
                     LDGQEVPEKPSIDLPIEVPRYEFNNKDQSPLAGESGETEYITEVYGNQQNPVDIDKKL
                     PNETGFSGNMVETEDTKEPEVLMGGQSESVEFTKDTQTGMSGQTTPQVETEDTKEPEV
                     LMGGQSESVEFTKDTQTGMSGQTTPQIETEDTKEPEVLMGGQSESVEFTKDTQTGMSG
                     QTTPQVETEDTKEPEVLMGGQSESVEFTKDTQTGMSGQTTPQIETEDTKEPEVLMGGQ
                     SESVEFTKDTQTGMSGFSETATVVEDTRPKLVFHFDNNEPKVEENREKPTKNITPILP
                     ATGDIENVLAFLGILILSVLSIFSLLKNKQSNKKV"
     repeat_unit     1327. .1457
                     /gene="prtF"
                     /note="repeat domain 1"
     repeat_unit     1631. .2170
                     /gene="prtF"
                     /note="repeat domain 2"
BASE COUNT      977 a    472 c    616 g    780 t
ORIGIN


alignment_scores:
            Quality:  633.50              Length:    779
              Ratio:  1.560                 Gaps:     30
 Percent Similarity:  52.118   Percent Identity: 26.059

alignment_block:
 US-09-494-297-2 x STRPRTNF   ..

 Align seg 1/1  to: STRPRTNF  from: 1  to: 2845

   20 SerLysAsnSerLysArgPheThrValThrLeuValGlyValPheLeuMe 36
      :::|||:::::::::|||||||:::|||||||||||||||||||||||::||
  494 ACAAAAAGAAAAAGGCGATTTGCTGTCACTTTAGTGGGAGTCTTTTTTAT 543

   36 tIlePheAlaLeuValThrSerMetValGlyAlaLysThrValPheGlyL 53
      |:::::::|||   :::   ::::::      ::::::::::::::::::
  544 GCTTTTGGCATGCGCGGGTGCTATCGGTTTTGGTCAAGTAGCCTATGCTG 593

   53 euValGluSerSerThrProAsnAlaIleAsnProAspSerSerSerGlu 69
         |||::::::::::|||:::      :::|||      :::   |||
  594 CCGATGAGAAGACTGTGCCGAGTCATAGTAGTCCA.....AATCCTGAG 637

   70 TyrArgTrpTyrGlyTyrGluSerTyrValArgGlyHisProTyrTyrLy 86
      :::   ||||||||||||:::::|||   :::   :::|||   |||::
  638 TTTCCTTGGTACGGTTATGATGCTTATGGTAAGGAATATCCTGGATATAA 687

   86 sGlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArgS 103
      :   :::         ||||||||||||||||||||:::||||||||||
  688 TATTTGGACTCGTTATCATGACTTGAGAGTAAATTTAAATGGGAGTCGGA 737

  103 erTyrGlnValTyrCysPheAsnLeuLysLysAlaProLeuGlySer 119
      ||||||||||||||||||||||:::::::::   :::|||      :::
  738 GCTACCAAGTTTATTGTTTTAATATTCAATCTAATTATCCTAGCCAAAAA 787

  120 AspSerServalLysLysTrpTyrLysLysHisAspGlyIleSerThrLy 136
      :::|||   :::|||:::|||:::||||||   :::|||   :::   ::
  788 AATAGTTTCATAAAAAATTGGTTTAAAAAAATTGAGGGAAATGGCAAATC 837

  136 sPheGluAspTyrAlaMetSerProArgIleThrGlyAspGluLeuAsnG 153
      :|||   |||||||||   :::   ::::::      :::||||||:::|
  838 CTTTGTAGATTATGCTCACACTACTAAACTAGGTAAAGAAGAGTTGGAGC 887

  153 lnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGly 169
      ||:::|||   :::::::::||||||:::::|||:::::|||||||||
  888 AGAGGCTCTTAAGTTTACTGTATAATGCGTATCCCAACGATGCTAATGGT 937

  170 IleMetGluGlyLeuGluProLeuAsnAlaIleArgValThrGlnGluAl 186
         |||:::|||||||||   ||||||||||||   |||||||||   ||
  938 TATATGAAAGGACTGGAGCATTTAAATGCTATTACTGTAACACAATATGC 987

  186 aValTrpTyrTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerP 203
      |||||||:::|||||||||||||:::      :::      :::      :
  988 AGTTTGGCATTACTCAGATAATTCACAATATCAATTT...GAGACATTAT 1034

  203 heLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeu 219
      :::::   |||:::::::::::::   :::|||   ||||||:::::|||
```